## SEQUENCE LISTING

<110> HAFEN, Ernst <120> In vivo model system for type-2 diabetes <130> 27656/38053 <140> To be determined <141> To be determined <150> PCT/IB99/01166 <151> 1999-06-22 <160> 4 <170> PatentIn Ver. 2.1 <210> 1 <211> 2907 <212> DNA <213> Drosophila melanogaster <400> 1 atggcatcaa tatcggatga cggcatggcg ctgagtggct acctcaagaa gctgaagacc 60 atgaagaaga agttetttgt getgtaegag gagaegagea etteggeage eeggetggag 120 tactacgata ccgaaaagaa gttcctgcaa agagccgagc caaaaagggt tatatatctg 180 aagaattgct tcaacatcaa tcgccgtttg gacaccaagc atagatttgt cattgtgctc 240 tcctccagag acggtggatt cggcatcgtt ctcgagaacg aaaatgattt acgcaaatgg 300 ttggacaaac tactagttet acaaaggaac atagecaatt egaatggaac agegeactea 360 ccttatgacc acgtttggca agttgtcatt caaaagaagg gtatttcgga gaaagttgga 420 atcaccggaa cctaccactg ttgccttact tcaaaatccc tgacattcgt gtgcattgga 480 ccggagaaga cgcccaatgg cgaggatcgc gttgcgagca ttgaaatact tttgaccacg 540 atcaggcgat gcggtcatgc atccccacaa tgtatattct acgtggaact tggccgccaa 600 agtgtcttgg gatctggtga tctgtggatg gagacggata acgcagctat tgctactaat 660 atgcacaca cgatactgag cgctatgtca gccaaaacag agtcgaacac gaatttaata 720 aacgtttatc agaatagacc tgacttaagt cacgagccca tgagaaagcg atcgtcgtct 780 gcaaacgaag catcgaagcc gataaacgta aatgtcatac aaaatagtca aaactctctc 840 gaattgcgca gctgcagttc gccccataac tatggtttcg gcagagagag atgcgatagc 900 ttaccaacca gaaatggaac cctaagcgag tccagcaatc aaacgtactt tggttccaac 960 catggactgc gatccaatac tatatctggc atccgtccgc actcaaccaa caagcatagt 1020 aatagteeaa egtteaceat geeattaaga tgeteagaat eegaagagte ateaattagt 1080 gtcgatgaat ccgacgacaa cggcagtttt agccactaca gattaaacac gcggtcatct 1140 gagacggcaa ttcctgagga aaacattgat gactttgcca gtgcggaatt atttagcaaa 1200 gtcaccgaac aaaatgtaag tgacgaaaac tacataccga tgaatccagt caatcctacc 1260 gatgctatcc atgaaaagga gaaggctgat atgcagagat tggaagatgc ttcgctgcat 1320 ttcaactttc cggagcacgc gtcggaaaag cttgctaagg attttgatct ggactctgat 1380 aaccaatget gtcgtcccat tcgcgcctat tcgataggca acaaggttga gcatttaaag 1440 tttaataagc gcctgggaca cttgaatgat acgggacaga atccgaatcg cgtgcgagcc 1500 tactcggttg gctccaaatc gaagataccg cgctgcgacc tgcagcgagt ggtcctcgtg 1560 gaggacaata aacatgagtt cacagcgaat aggagtcaga gtagcattac caaggaagga 1620 accagctatg gcagcagtgc caatcgacaa aagaagtcca caagtgctcc actcctcagt 1680 ctgaagaacc agataaactc cgaccgaatg agtgacttaa tggaaattga tttttcacaa 1740 gcaaccaatt tggaaaagca gaagttcatc aagaataatg aaattccgaa atacattgaa 1800 aacgtgttcc caaaagcccc gcgaacggat agctccagcc taactctgca cgccacaagt 1860 caaaaggaca ttttcaatgg caccaaacta aataacactg cgatcacatc cgaggatggt 1920 tacctcgaga tgaagccagt cggtaatgga tacactccca gttcgaattg cctgccaatg 1980 aaagtggaga aactcaagct atccgactat cagacagcac cgccactcac cgcaacagcc 2040 gcaccagtgc acgatttaaa caaaattagc acatacaata tatccgctga gaaatggaga 2100 gaacagccca gcagaagcga ggaaaagaag tcgaactcgc cattgaatga caacaccttt 2160 agctcgaaac ccacaaatgt cgagagtaca agcaaaagcc atgatgttca ttcagcaaat 2220 caaattgatt gcgagaaagt gtgcgcgcag agcagcgata agctaaataa tcatctggcc 2280 gacaagattg togagaacaa caatttggat ataggogggo atgaggaaaa gaagttggtt 2340 cattcgataa gcagcgaaga ctacacacaa atcaaggaca aatcgaatga tttcacaaaa 2400 tttaacgaag ccggctacaa aattctgcaa attaaaagcg acagctcact catctcatcg 2460 aagctatacc aaaagggtat acacaaggat aacttggagc gttcgcagag acttacagag 2520 agtgtgaata cgattcccga taatgccacc gccaccgcgg tgagcagcag ctcactcacc 2580 aaattcaata taaattcagc aaagccagcc gccgccgccg attcgcgtag cactggcaca 2640 gatccaagta caccacagaa cattctacag attaaagatt tgaatttccc ctcaaggtcg 2700 tegtetegea tateceagee ggagetgeae taegeeagee tagatettee ceattgeagt 2760 ggccaaaatc cagctaaata cctgaagaga ggatcacgcg aatcgccgcc ggtgtccgca 2820 tgcccggagg atgggaatac ctatgcgaaa atcgactttg accaatccga ctcctcttcc 2880 2907 tcctcatcga acatatttaa tacgtaa

<210> 2 <211> 2907 <212> DNA <213> Drosophila melanogaster																
<220> <221> CDS <222> (1)(2907)																
<400 atg Met 1	aca	tca Ser	ata Ile	tcg Ser 5	gat Asp	gac Asp	ggc Gly	atg Met	gcg Ala 10	ctg Leu	agt Ser	ggc Gly	tac Tyr	ctc Leu 15	aag Lys	48
aag Lys	ctg Leu	aag Lys	acc Thr 20	atg Met	aag Lys	aag Lys	aag Lys	ttc Phe 25	ttt Phe	gtg Val	ctg Leu	tac Tyr	gag Glu 30	gag Glu	acg Thr	96
agc Ser	act Thr	tcg Ser 35	gca Ala	gcc Ala	cgg Arg	ctg Leu	gag Glu 40	tac Tyr	tac Tyr	gat Asp	acc Thr	gaa Glu 45	aag Lys	aag Lys	ttc Phe	144
ctg Leu	caa Gln 50	aga Arg	gcc Ala	gag Glu	cca Pro	aaa Lys 55	agg Arg	gtt Val	ata Ile	tat Tyr	ctg Leu 60	aag Lys	aat Asn	tgc Cys	ttc Phe	192
aac Asn 65	atc Ile	aat Asn	cgc Arg	cgt Arg	ttg Leu 70	gac Asp	acc Thr	aag Lys	cat His	aga Arg 75	ttt Phe	gtc Val	att Ile	gtg Val	ctc Leu 80	240
tcc Ser	tcc Ser	aga Arg	gac Asp	ggt Gly 85	gga Gly	ttc Phe	ggc Gly	atc Ile	gtt Val 90	ctc Leu	gag Glu	aac Asn	gaa Glu	aat Asn 95	gat Asp	288
tta Leu	cgc Arg	aaa Lys	tgg Trp 100	ttg Leu	gac Asp	aaa Lys	cta Leu	cta Leu 105	gtt Val	cta Leu	caa Gln	agg Arg	aac Asn 110	ata Ile	gcc Ala	336
aat Asn	tcg Ser	aat Asn 115	gga Gly	aca Thr	gcg Ala	cac His	tca Ser 120	cct Pro	tat Tyr	gac Asp	cac His	gtt Val 125	tgg Trp	caa Gln	gtt Val	384
gtc Val	att Ile 130	Gln	Lys	Lys	Gly	Ile	Ser	Glu	aaa Lys	Val	Gly	Ile	acc Thr	gga Gly	acc Thr	432
tac Tyr 145	cac His	tgt Cys	tgc Cys	ctt Leu	act Thr 150	Ser	aaa Lys	tcc Ser	ctg Leu	aca Thr 155	Phe	gtg Val	tgc Cys	att Ile	gga Gly 160	480
ccg Pro	gag Glu	aag Lys	acg Thr	ccc Pro 165	Asn	ggc Gly	gag Glu	gat Asp	cgc Arg 170	gtt Val	gcg Ala	agc Ser	att Ile	gaa Glu 175	ata Ile	528
ctt Leu	ttg Leu	acc Thr	acg Thr 180	Ile	agg Arg	cga Arg	tgc Cys	ggt Gly 185	cat His	gca Ala	tcc Ser	cca Pro	caa Gln 190	. Cys	ata Ile	576
ttc Phe	tac Tyr	gtg Val 195	Glu	ctt Leu	ggc Gly	cgc Arg	caa Gln 200	Ser	gtc Val	ttg Leu	gga Gly	tct Ser 205	GTA	gat Asp	ctg Leu	624

tgg Trp	atg Met 210	gag Glu	acg Thr	gat Asp	aac Asn	gca Ala 215	gct Ala	att Ile	gct Ala	act Thr	aat Asn 220	atg Met	cac His	aac Asn	acg Thr	672
ata Ile 225	ctg Leu	agc Ser	gct Ala	atg Met	tca Ser 230	gcc Ala	aaa Lys	aca Thr	gag Glu	tcg Ser 235	aac Asn	acg Thr	aat Asn	tta Leu	ata Ile 240	720
aac Asn	gtt Val	tat Tyr	cag Gln	aat Asn 245	aga Arg	cct Pro	gac Asp	tta Leu	agt Ser 250	cac His	gag Glu	ccc Pro	atg Met	aga Arg 255	aag Lys	768
cga Arg	tcg Ser	tcg Ser	tct Ser 260	gca Ala	aac Asn	gaa Glu	gca Ala	tcg Ser 265	aag Lys	ccg Pro	ata Ile	aac Asn	gta Val 270	aat Asn	gtc Val	816
ata Ile	caa Gln	aat Asn 275	agt Ser	caa Gln	aac Asn	tct Ser	ctc Leu 280	gaa Glu	ttg Leu	cgc Arg	agc Ser	tgc Cys 285	agt Ser	tcg Ser	ccc Pro	864
cat His	aac Asn 290	tat Tyr	ggt Gly	ttc Phe	ggc Gly	aga Arg 295	gag Glu	aga Arg	tgc Cys	gat Asp	agc Ser 300	tta Leu	cca Pro	acc Thr	aga Arg	912
aat Asn 305	gga Gly	acc Thr	cta Leu	agc Ser	gag Glu 310	tcc Ser	agc Ser	aat Asn	caa Gln	acg Thr 315	tac Tyr	ttt Phe	ggt Gly	tcc Ser	aac Asn 320	960
cat His	gga Gly	ctg Leu	cga Arg	tcc Ser 325	aat Asn	act Thr	ata Ile	tct Ser	ggc 330	atc Ile	cgt Arg	ccg Pro	cac His	tca Ser 335	acc Thr	1008
aac Asn	aag Lys	cat His	agt Ser 340	aat Asn	agt Ser	cca Pro	acg Thr	ttc Phe 345	acc Thr	atg Met	cca Pro	tta Leu	aga Arg 350	tgc Cys	tca Ser	1056
gaa Glu	tcc Ser	gaa Glu 355	Glu	tca Ser	tca Ser	att Ile	agt Ser 360	gtc Val	gat Asp	gaa Glu	tcc Ser	gac Asp 365	gac Asp	aac Asn	ggc	1104
agt Ser	ttt Phe 370	agc Ser	cac His	tac Tyr	aga Arg	tta Leu 375	Asn	acg Thr	cgg Arg	tca Ser	tct Ser 380	Glu	acg Thr	gca Ala	att Ile	1152
cct Pro 385	Glu	gaa Glu	aac Asn	att Ile	gat Asp 390	Asp	ttt Phe	gcc Ala	agt Ser	gcg Ala 395	Glu	tta Leu	ttt Phe	ago Ser	aaa Lys 400	1200
gto Val	acc Thr	gaa Glu	caa Gln	aat Asn 405	Val	agt Ser	gac Asp	gaa Glu	aac Asn 410	ı Tyr	ata Ile	ccg Pro	atg Met	aat Asn 415	cca Pro	1248
gto Val	aat Asn	cct Pro	acc Thr	Asp	gct Ala	ato Ile	cat His	gaa Glu 425	Lys	gag Glu	g aag Lys	gct Ala	gat Asp 430	Met	g cag : Gln	1296
aga Arg	ttg Lev	gaa Glu 435	ı Asp	gct Ala	tcg Ser	r ctg	cat His	Phe	aac Asr	ttt 1 Phe	ccg Pro	g gag Glu 445	ı Hıs	gcg Ala	tcg Ser	1344
gaa Glu	a aag 1 Lys 450	: Le	gct 1 Ala	aag Lys	gat Asp	ttt Phe 455	e Asp	cto Lei	g gad 1 Asp	c tct Sei	gat Ası 460	o Asr	c caa n Glr	tgo Cys	tgt Cys	1392

cgt Arg 465	ccc Pro	att Ile	cgc Arg	gcc Ala	tat Tyr 470	tcg Ser	ata Ile	ggc Gly	aac Asn	aag Lys 475	gtt Val	gag Glu	cat His	tta Leu	aag Lys 480	1440
ttt Phe	aat Asn	aag Lys	cgc Arg	ctg Leu 485	gga Gly	cac His	ttg Leu	aat Asn	gat Asp 490	acg Thr	gga Gly	cag Gln	aat Asn	ccg Pro 495	aat Asn	1488
cgc Arg	gtg Val	cga Arg	gcc Ala 500	tac Tyr	tcg Ser	gtt Val	ggc Gly	tcc Ser 505	aaa Lys	tcg Ser	aag Lys	ata Ile	ccg Pro 510	cgc Arg	tgc Cys	1536
gac Asp	ctg Leu	cag Gln 515	cga Arg	gtg Val	gtc Val	ctc Leu	gtg Val 520	gag Glu	gac Asp	aat Asn	aaa Lys	cat His 525	gag Glu	ttc Phe	aca Thr	1584
gcg Ala	aat Asn 530	agg Arg	agt Ser	cag Gln	agt Ser	agc Ser 535	att Ile	acc Thr	aag Lys	gaa Glu	gga Gly 540	acc Thr	agc Ser	tat Tyr	ggc Gly	1632
agc Ser 545	agt Ser	gcc Ala	aat Asn	cga Arg	caa Gln 550	aag Lys	aag Lys	tcc Ser	aca Thr	agt Ser 555	gct Ala	cca Pro	ctc Leu	ctc Leu	agt Ser 560	1680
ctg Leu	aag Lys	aac Asn	cag Gln	ata Ile 565	aac Asn	tcc Ser	gac Asp	cga Arg	atg Met 570	agt Ser	gac Asp	tta Leu	atg Met	gaa Glu 575	att Ile	1728
gat Asp	ttt Phe	tca Ser	caa Gln 580	gca Ala	acc Thr	aat Asn	ttg Leu	gaa Glu 585	aag Lys	cag Gln	aag Lys	ttc Phe	atc Ile 590	aag Lys	aat Asn	1776
aat Asn	gaa Glu	att Ile 595	ccg Pro	aaa Lys	tac Tyr	att Ile	gaa Glu 600	aac Asn	gtg Val	ttc Phe	cca Pro	aaa Lys 605	gcc Ala	ccg Pro	cga Arg	1824
acg Thr	gat Asp 610	agc Ser	tcc Ser	agc Ser	cta Leu	act Thr 615	ctg Leu	cac His	gcc Ala	aca Thr	agt Ser 620	caa Gln	aag Lys	gac Asp	att Ile	1872
ttc Phe 625	aat Asn	ggc Gly	acc Thr	aaa Lys	cta Leu 630	aat Asn	aac Asn	act Thr	gcg Ala	atc Ile 635	aca Thr	tcc Ser	gag Glu	gat Asp	ggt Gly 640	1920
tac Tyr	ctc Leu	gag Glu	atg Met	aag Lys 645	cca Pro	gtc Val	ggt Gly	aat Asn	gga Gly 650	tac Tyr	act Thr	ccc Pro	agt Ser	tcg Ser 655	aat Asn	1968
tgc Cys	ctg Leu	cca Pro	atg Met 660	aaa Lys	gtg Val	gag Glu	aaa Lys	ctc Leu 665	aag Lys	cta Leu	tcc Ser	gac Asp	tat Tyr 670	cag Gln	aca Thr	2016
gca Ala	ccg Pro	cca Pro 675	ctc Leu	acc Thr	gca Ala	aca Thr	gcc Ala 680	gca Ala	cca Pro	gtg Val	cac His	gat Asp 685	tta Leu	aac Asn	aaa Lys	2064
att Ile	agc Ser 690	aca Thr	tac Tyr	aat Asn	ata Ile	tcc Ser 695	gct Ala	gag Glu	aaa Lys	tgg Trp	aga Arg 700	gaa Glu	cag Gln	ccc Pro	agc Ser	2112
aga Arg 705	agc Ser	gag Glu	gaa Glu	aag Lys	aag Lys 710	tcg Ser	aac Asn	tcg Ser	cca Pro	ttg Leu 715	aat Asn	gac Asp	aac Asn	acc Thr	ttt Phe 720	2160

_	_				aat Asn	_		_		_		_		_	_	2208
		_			att Ile	_	_				_		_	_	_	2256
					cat His											2304
					cat His											2352
-	_	_			caa Gln 790		_	_		_		_				2400
		-	-		tac Tyr			_				_	_	_		2448
			_	_	cta Leu			_				_	_		_	2496
	_	_	_	_	ctt Leu			_			_			_		2544
_		_			gtg Val	_	_	_								2592
					gcc Ala 870											2640
_		_			cag Gln				_			_	_			2688
					tct Ser											2736
					cat His											2784
					gaa Glu											2832
					aaa Lys 950											2880
					ttt Phe			taa								2907

<210> 3 <211> 968 <212> PRT <213> Drosophila melanogaster															
	0> 3 Ala	Ser	Ile	Ser 5	Asp	Asp	Gly	Met	Ala 10	Leu	Ser	Gly	Tyr	Leu 15	Lys
Lys	Leu	Lys	Thr 20	Met	Lys	Lys	Lys	Phe 25	Phe	Val	Leu	Tyr	Glu 30	Glu	Thr
Ser	Thr	Ser 35	Ala	Ala	Arg	Leu	Glu 40	Tyr	Tyr	Asp	Thr	Glu 45	Lys	Lys	Phe
Leu	Gln 50	Arg	Ala	Glu	Pro	Lys 55	Arg	Val	Ile	Tyr	Leu 60	Lys	Asn	Cys	Phe
Asn 65	Ile	Asn	Arg	Arg	Leu 70	Asp	Thr	Lys	His	Arg 75	Phe	Val	Ile	Val	Leu 80
Ser	Ser	Arg	Asp	Gly 85	Gly	Phe	Gly	Ile	Val 90	Leu	Glu	Asn	Glu	Asn 95	Asp
Leu	Arg	Lys	Trp 100	Leu	Asp	Lys	Leu	Leu 105	Val	Leu	Gln	Arg	Asn 110	Ile	Ala
Asn	Ser	Asn 115	Gly	Thr	Ala	His	Ser 120	Pro	Tyr	Asp	His	Val 125	Trp	Gln	Val
Val	Ile 130	Gln	Lys	Lys	Gly	Ile 135	Ser	Glu	Lys	Val	Gly 140	Ile	Thr	Gly	Thr
Tyr 145	His	Cys	Cys	Leu	Thr 150	Ser	Lys	Ser	Leu	Thr 155	Phe	Val	Cys	Ile	Gly 160
Pro	Glu	Lys	Thr	Pro 165	Asn	Gly	Glu	Asp	Arg 170	Val	Ala	Ser	Ile	Glu 175	Ile
Leu	Leu	Thr	Thr 180	Ile	Arg	Arg	Cys	Gly 185	His	Ala	Ser	Pro	Gln 190	Cys	Ile
Phe	Tyr	Val 195	Glu	Leu	Gly	Arg	Gln 200	Ser	Val	Leu	Gly	Ser 205	Gly	Asp	Leu
Trp	Met 210	Glu	Thr	Asp	Asn	Ala 215	Ala	Ile	Ala	Thr	Asn 220	Met	His	Asn	Thr
Ile 225	Leu	Ser	Ala	Met	Ser 230	Ala	Lys	Thr	Glu	Ser 235	Asn	Thr	Asn	Leu	Ile 240
Asn	Val	Tyr	Gln	Asn 245	Arg	Pro	Asp	Leu	Ser 250	His	Glu	Pro	Met	Arg 255	Lys
Arg	Ser	Ser	Ser 260	Ala	Asn	Glu	Ala	Ser 265	Lys	Pro	Ile	Asn	Val 270	Asn	Val
Ile	Gln	Asn 275	Ser	Gln	Asn	Ser	Leu 280	Glu	Leu	Arg	Ser	Cys 285	Ser	Ser	Pro
His	Asn 290	Tyr	Gly	Phe	Gly	Arg 295	Glu	Arg	Cys	Asp	Ser 300	Leu	Pro	Thr	Arg

Asn Gly Thr Leu Ser Glu Ser Ser Asn Gln Thr Tyr Phe Gly Ser Asn His Gly Leu Arg Ser Asn Thr Ile Ser Gly Ile Arg Pro His Ser Thr 330 325 Asn Lys His Ser Asn Ser Pro Thr Phe Thr Met Pro Leu Arg Cys Ser Glu Ser Glu Glu Ser Ser Ile Ser Val Asp Glu Ser Asp Asp Asn Gly Ser Phe Ser His Tyr Arg Leu Asn Thr Arg Ser Ser Glu Thr Ala Ile Pro Glu Glu Asn Ile Asp Asp Phe Ala Ser Ala Glu Leu Phe Ser Lys Val Thr Glu Gln Asn Val Ser Asp Glu Asn Tyr Ile Pro Met Asn Pro Val Asn Pro Thr Asp Ala Ile His Glu Lys Glu Lys Ala Asp Met Gln Arg Leu Glu Asp Ala Ser Leu His Phe Asn Phe Pro Glu His Ala Ser Glu Lys Leu Ala Lys Asp Phe Asp Leu Asp Ser Asp Asn Gln Cys Cys 455 Arg Pro Ile Arg Ala Tyr Ser Ile Gly Asn Lys Val Glu His Leu Lys Phe Asn Lys Arg Leu Gly His Leu Asn Asp Thr Gly Gln Asn Pro Asn Arg Val Arg Ala Tyr Ser Val Gly Ser Lys Ser Lys Ile Pro Arg Cys 505 Asp Leu Gln Arg Val Val Leu Val Glu Asp Asn Lys His Glu Phe Thr Ala Asn Arg Ser Gln Ser Ser Ile Thr Lys Glu Gly Thr Ser Tyr Gly 530 Ser Ser Ala Asn Arg Gln Lys Lys Ser Thr Ser Ala Pro Leu Leu Ser Leu Lys Asn Gln Ile Asn Ser Asp Arg Met Ser Asp Leu Met Glu Ile Asp Phe Ser Gln Ala Thr Asn Leu Glu Lys Gln Lys Phe Ile Lys Asn 585 Asn Glu Ile Pro Lys Tyr Ile Glu Asn Val Phe Pro Lys Ala Pro Arg 600 Thr Asp Ser Ser Ser Leu Thr Leu His Ala Thr Ser Gln Lys Asp Ile Phe Asn Gly Thr Lys Leu Asn Asn Thr Ala Ile Thr Ser Glu Asp Gly 625 630 635

Tyr Leu Glu Met Lys Pro Val Gly Asn Gly Tyr Thr Pro Ser Ser Asn Cys Leu Pro Met Lys Val Glu Lys Leu Lys Leu Ser Asp Tyr Gln Thr 665 Ala Pro Pro Leu Thr Ala Thr Ala Ala Pro Val His Asp Leu Asn Lys Ile Ser Thr Tyr Asn Ile Ser Ala Glu Lys Trp Arg Glu Gln Pro Ser Arg Ser Glu Glu Lys Lys Ser Asn Ser Pro Leu Asn Asp Asn Thr Phe Ser Ser Lys Pro Thr Asn Val Glu Ser Thr Ser Lys Ser His Asp Val 730 His Ser Ala Asn Gln Ile Asp Cys Glu Lys Val Cys Ala Gln Ser Ser Asp Lys Leu Asn Asn His Leu Ala Asp Lys Ile Val Glu Asn Asn Asn Leu Asp Ile Gly Gly His Glu Glu Lys Lys Leu Val His Ser Ile Ser Ser Glu Asp Tyr Thr Gln Ile Lys Asp Lys Ser Asn Asp Phe Thr Lys Phe Asn Glu Ala Gly Tyr Lys Ile Leu Gln Ile Lys Ser Asp Ser Ser Leu Ile Ser Ser Lys Leu Tyr Gln Lys Gly Ile His Lys Asp Asn Leu Glu Arg Ser Gln Arg Leu Thr Glu Ser Val Asn Thr Ile Pro Asp Asn 840 Ala Thr Ala Thr Ala Val Ser Ser Ser Leu Thr Lys Phe Asn Ile Asn Ser Ala Lys Pro Ala Ala Ala Ala Asp Ser Arg Ser Thr Gly Thr 870 875 Asp Pro Ser Thr Pro Gln Asn Ile Leu Gln Ile Lys Asp Leu Asn Phe Pro Ser Arg Ser Ser Arg Ile Ser Gln Pro Glu Leu His Tyr Ala Ser Leu Asp Leu Pro His Cys Ser Gly Gln Asn Pro Ala Lys Tyr Leu 920 Lys Arg Gly Ser Arg Glu Ser Pro Pro Val Ser Ala Cys Pro Glu Asp Gly Asn Thr Tyr Ala Lys Ile Asp Phe Asp Gln Ser Asp Ser Ser Ser Ser Ser Ser Asn Ile Phe Asn Thr 965

<210> 4 <211> 5210 <212> DNA

<213> Drosophila melanogaster

<400> 4

agaacgactt tttcctcctt agtcagtcac aagaaaacta aagcttacca acaatacggc 60 gtgtattgtt aaattattac aacaaataaa atattcaaat tgtatttaaa aatatagtaa 120 ccattaaaaa ataaaatcaa tatgcgaaac tttgtaattt cttactcatc cttgttttt 180 gagcccgctt tcttaagtta aatcgttaaa ataccagttt aatcatttca ttgtcctgat 240 ttcaggagct aattacattt taatctttgt ataaattcat aaaattaaaa tggaaatgtt 300 taaccacata aaatatttgg gtatataaag tcgatacata cttttaaaat tttgtttcat 360 acaagaatat ggaaagtaga taatttagtt accgattaaa acatttctaa aatacaaaaa 420 atttaaaatg atgattaaat aaaaaactgt tatactaaat ttaaacgaaa caaacggtca 480 ttcgataact caattagtat cgaataagcc ggcgtgtaaa tcgggttggc aactctcacc 540 ggtgtagaga tcgggatggc aacttcgtat tgttattcct atgctgcgat aacgataaca 600 gcaaagtgtc atcgcgaata aatgtgggtt tgataataaa gaattgcgtt ggtgaacaat 660 aataatacaa atgctaaatg tatcgcgcgg ataactagta aacactgatt tcgcgcatat 720 cgggcatacg ggcagctaga cgtcttaggt aacacatttc ccagccacat tggcgttgag 780 gtattattte ecatatecat gtgegtttgt aaatgatace accagagtgt gecatatgta 840 tcgttgtttg tacatacatg cctacgggga aaaataactc gcagatacat atgtatgtaa 900 gatgtattag aattccacag atatatgtac atataaatat atatatat ttatgatgct 960 catctataaa acaaaatatg tacaaacata cgcgcgcacg tacttatgta tgtacatata 1020 gcagaaacct gaaaacgaaa taaacaatct ttacagcgcc agcacagtga gccaattatg 1140 aattcacaat tccacatcca attccgattc cgaattccat cgctttacat cctaattcga 1200 atacgtcgcg ccgcgtaagc tgcactcgaa tattgacata aacgacgtaa ttgcgtgttt 1260 tgattgcgat ttccgatgct cgatgttgac agacggcaag gatttttttt gccagccgac 1320 attgcgaatg cttttcgcgt gtttgcgttg tgaaaagcga tttgttgttc cggcagttgg 1380 aaatgttttg tgctgtttat gcttagaaaa gcaaatgtat tgcacaaaac tcgtgtttcc 1440 tacattagta aagcctataa cttaggtata tgtttctaaa ttacaatgca aaaaataaaa 1500 aacattatac atgtgttcgt tctttaattt gaaaacagaa aagtgaaagc cttgcaaatc 1560 aaatatgtgt ccatatcgcc tactaataat ataaacacgt cgccttccag gaactaagat 1620 tggaaatcat ggcatcaata tcggatgacg gcatggcgct gagtggctac ctcaagaagc 1680 tgaagaccat gaagaagaag ttctttgtgc tgtacgagga gacgagcact tcggcagccc 1740 ggctggagta ctacgatacc gaaaagaagt tcctgcaaag agccgagcca aaaagggtta 1800 tctatctgaa gaattgcttc aacatcaatc gccgtttgga caccaagcat agatttgtca 1860 ttgtgctctc ctccagagac ggtggattcg gcatcgttct cgagaacgaa aatgatttac 1920 gcaaatggtt ggacaaacta ctagttctac aaaggaacat agccaattcg aatggaacag 1980 cgcactcacc ttatggtatg ccaaataaac tataactacc agttagtatg aaacctaaac 2040 acttcatttc actttgcaga ccacgtttgg caagttgtca ttcaaaagaa gggtatttcg 2100 gagaaagttg gaatcaccgg aacctaccac tgttgcctta cttcaaaatc cctgacattc 2160 gtgtgcattg gaccggagaa gacgcccaat ggcgaggatc gcgttgcgag cattgaaata 2220 cttttgacca cgatcaggcg gttagttgtt gccagcaaaa ctgcaaggga ttgtaaaata 2280 atteggaett aattteagat geggteatge ateceeacaa tgtatattet aegtggaaet 2340 tggccgccaa agtgtcttgg gatctggtga tctgtggatg gagacggata acgcagctat 2400 tgctactaat atgcacaaca cgatactgag gtatttagct ctcattacaa ctaatccaag 2460 atttcatgat catcctacaa aacgacatag atagtttaag atatctccca gttaacttta 2520 ataattetgt gggtttttte ttteageget atgteageea aaacagagte gaacaegaat 2580 ttaataaacg tttatcagaa cagacctgac ttaagtcacg agcccatgag aaagcgatcg 2640 tcgtctgcaa acgaagcatc gaagccgata aacgtaaatg tcatacaaaa tagtcaaaac 2700 tototogaat tgcgcagetg cagttcgccc cataactatg gtaaatactt caaatgtatg 2760 tttaaacgca aaattaatca aacgcaatcg tttcaggttt cggcagagag agatgcgata 2820 gettaccaac cagaaatgga accetaageg agtecageaa teaaaegtae tttggtteea 2880 accatggact gcgatccaat actatatctg gcatccgtcc gcactcaacc aacaagcata 2940 gtaatagtcc aacgttcacc atgccattaa gatgctcaga atccgaagag tcatcaatta 3000 gtgtcgatga atccgacgac aacggcagtt ttagccacta cagattaaag tgcgttgcta 3060 tcaaataata attatttaat aataatcacc atttcaattt ctagcacgcg gtcatctgag 3120 acggcaattc ctgaggaaaa cattgatgac tttgccagtg cggaattatt tagcaaagtc 3180 accgaacaaa atggtaagcc aaacacaaaa acaatttttt aacatgaaaa gtagctaatc 3240 aattggcttt gtttaactgc agtaagtgac gaaaactaca taccgatgaa tccagtcaat 3300 cctaccgatg ctatccatga aaaggagaag gctgatatgc agagattgga agatgcttcg 3360 ctgcatttca actttccgga gcacgcgtcg gaaaagcttg ctaaggattt tgatctggac 3420 totgataacc agtgagtaca catttegett caactgtgee acgtaatgea atcaatcaca 3480 tettgttaca gatgetgteg teccattege geetattega taggeaacaa ggttgageat 3540 ttaaagttta ataagcgcct gggacacttg aatgatacgg gacagaatcc gaatcgcgtg 3600 cgagcctact cggttggctc caaatcgaag ataccgcgct gcgacctgca gcgagtggtc 3660 ctcgtggagg acaataaaca tgagttcaca gcgaatagga gtcagagtag cattaccaag 3720 gaaggaacca gctatggcag cagtgccaat cgacaaaaga agtccacaag tgctccactc 3780 ctcagtctga agaaccagat aaactccgac cgaatgagtg acttaatgga aattgatttt 3840 tcacaagcaa ccaatttgga aaagcagaag ttcatcaaga ataatgaaat tccgaaatac 3900 attgaaaacg tgttcccaaa agccccgcga acggatagct ccagcctaac tctgcacgcc 3960 acaagtcaaa aggacatttt caatggcacc aaactaaata acactgcgat cacatccgag 4020 gatggttacc tegagatgaa gecagteggt aatggataca eteceagtte gaattgeetg 4080 ccaatgaaag tggagaggct caagctatcc gactatcaga cagcaccgcc aatcaccgca 4140 acageegeae eagtgeaega tttaaaeaaa attageaeat acaatatate egetgagaaa 4200 tggagagaac agcccagcag aagcgaggaa aagaagtcga actcgccatt gaatgacaac 4260 acctttggct tgaaacccac aaatgtcgag agtacaagca aaagccatga tgttcattca 4320 gcaaatcaaa ttgattccga gaaagtgtgc gcgcagagca gcgataagct aaataatctg 4380 gccgacaaga ttgtcgagaa caacaatttg gatataggcg ggcatgagga aaagaagttg 4440 gttcattcga taagcagcga agactacaca caaatcaagg acaaatcgaa tgatttcaca 4500 aaatttaacg aagccggcta caaaattctg caaattaaaa gcgacagctc actcatctca 4560 tegaagetat accaaaaggg tatacacaag gataaettgg agegttegea gagaettaeg 4620 gagagtgtga atacgattcc cgataatgcc accgccaccg cggtgagcag cagctcactc 4680 accaaattca atataaattc agcaaagcca gccgccgccg ccgattcgcg tagcactggc 4740 acagatecaa gtacaccaca gaacatteta cagattaaag atttgaattt cecetcaagg 4800 tegtegtete geatateeca geeggagetg caetaegeea geetagatet teeceattge 4860 agtggccaaa atccagctaa atacctgaag agaggatcac gcgaatcgcc gccggtgtcc 4920 gcatgcccgg aggatgggaa tacctatgcg aaaatcgact ttgaccaatc cgactcctct 4980 tectecteat egaacatatt taataegtaa agttttgaaa tttatgaeee tateetatat 5040 atatgatttg tttaatattg tacatttatt gtaaatattc tctgacaagc aaagcttaca 5100 attttggatg ctaataaata aattttattt aaattataat gatccctttg gacttttttt 5160 ttttttggac taagaaatca ctactaaaga agggcttttc gagggttaaa 5210